Chapter 10

Conformations
Conformations

- Identical Composition
- Identical Connection Pattern
- Different bond length
- Different angles
- Different dihedrals
Stochastic Conformational Search

The Stochastic Conformational Search algorithm proceeds as follows:

1. Initialize the conformer list to empty and identify all rotation bonds.
2. Randomly invert all chiral centers for which there is no chiral constraint applied. This will ensure sampling of easily invertible chiral centers (e.g., chiral centers with lone pairs).
3. Rotate all rotation bonds (including ring bonds) to random dihedral angles (possibly biased towards certain multiples of 30 or 60 degrees).
4. Energy minimize the resulting conformation in dihedral angle space; that is, minimize energy by rotating bonds without changing bond lengths or angles.
5. Perturb all atom positions by plus or minus delta (the specified position perturbation); the sign is determined randomly.
6. Minimize energy in Cartesian coordinates until the RMS gradient is equal to or below the Gradient Test parameter.
7. Check for duplicates in the conformer list. Compare the relative atomic positions of the latest conformation with all conformations previously saved. If the atom positions of the current conformer are within the RMS Tolerance of the atom positions of a saved conformer, discard the current conformation and increment the failure count. If no duplicate was found, put the current conformation into the list and set the failure count to zero.
8. If the failure count exceeds the Failure Limit parameter then stop. If the iteration count exceeds the Iteration Limit parameter then stop.
9. Return to Step 3.
Running the Search

- MOE | Compute | Conformations | Stochastic Search

![Stochastic Conformational Search dialog box]

- Output Database: `scsearch.mdl`
- Conformation Generation:
  - Chiral Inversion
  - Bond Rotation (Mode: `bias-30`)
  - Dihedral Minimization (RMS Gradient: 100)
  - Cartesian Perturbation (Delta: 0.0001)
  - Cartesian Minimization (RMS Gradient: 0.001)
- Energy Cutoff: 7
- Failure Limit: 20
- RMS Tolerance: 0.1
- Conformation Limit: 10000
- Iteration Limit: 10000
- MM Iteration Limit: 200

Options:
- Add Chiral Constraints
- Rotate Amide Bonds
- Rotate Double Bonds
- Calculate Forcefield Partial Charges

[OK] [Cancel]
## Output

<table>
<thead>
<tr>
<th>Field</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mol</td>
<td>A molecular conformation</td>
</tr>
<tr>
<td>E</td>
<td>The potential energy of the conformation (in kcal/mol) determined by the Potential Setup window</td>
</tr>
<tr>
<td>dE</td>
<td>The strain energy of the conformation (in kcal/mol). This is defined to be the energy of the conformation minus the smallest conformational energy seen within the chiral class (enantiomer class) annotated in the chi field</td>
</tr>
<tr>
<td>Chi</td>
<td>An integer indicating the chiral class of the conformation. If the molecule contains ( k ) unconstrained chiral centers then there will be up to ( 2k ) chiral classes numbered 1,2,...</td>
</tr>
</tbody>
</table>
Conformations of Butane

- 180°  -5.0348 kcal/mol
- -65.2° -4.2554 kcal/mol
- 65.2° -4.2554 kcal/mol
Dihedral Energy Plot

- MOE | Compute | Mechanics | Dihedral Energy Plot

- Mark the four carbon atoms in butane
- Compare the result with the Stochastic Conformation Search